**Validated By CRFValidator v 1.0.3**

Application No: 09763824 Version No: 4.0

**Input Set:**

**Output Set:**

**Started:** 2007-09-14 09:36:59.177
**Finished:** 2007-09-14 09:37:01.124
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 947 ms
**Total Warnings:** 36
**Total Errors:** 0
**No. of SeqIDs Defined:** 42
**Actual SeqID Count:** 42

| Error code | | Error Description |
|---|---|---|
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (1) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (2) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (3) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (4) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (8) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (9) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (10) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (11) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (12) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (13) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (14) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (15) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (16) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (17) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (18) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (19) |
| W | 213 | Artificial or Unknown found in <213> in SEQ ID (20) |

**Input Set:**

**Output Set:**

**Started:** 2007-09-14 09:36:59.177
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**Total Warnings:** 36
**Total Errors:** 0
**No. of SeqIDs Defined:** 42
**Actual SeqID Count:** 42

| Error code | Error Description |
|---|---|

This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> SQUIRRELL, DAVID J.
MURPHY, MELANIE J.
PRICE, RACHEL L.
LOWE, CHRISTOPHER R.
WHITE, PETER J.
TISI, LAURENCE C.
MURRAY, JAMES A.H.

<120> NOVEL ENZYME

<130> 1498-119

<140> 09763824
<141> 2001-02-27

<150> PCT/GB99/03538
<151> 1999-10-26

<150> GB 9823468.5
<151> 1998-10-28

<160> 42

<170> PatentIn Ver. 2.1

<210> 1
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 1
cgccggtgag ctccccgccg ccg 23

<210> 2
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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cggcggcggg gagctcaccg gcg 23

<210> 3
<211> 51

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 3
cgaacacttc ttcatcgttg accgccttaa gtctttaatt aaatacaaag g 51

<210> 4
<211> 51
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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<210> 5
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 5
gaaaggcccg gcaccagcct atcctctaga gg 32

<210> 6
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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ccataaattt accgaattcg tcgacttcga tcgagg 36

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
gtgtggaatt gtgagcgg 18

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
gagatacgcc gcggttcctg g 21

<210> 10
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 10
ccaggaaccg cggcgtatct c 21

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccctattttc attcctggcc aaaagcactc 30

<210> 12
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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gagtgctttt ggccaggaat gaaaataggg 30

<210> 13
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
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<210> 14
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 14
gaatctgacg cagagagctc tatgcgg 27

<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
gttgaccgct tgggatcctt aattaaatac 30

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
gtatagattt gaaaaagagc tg 22

<210> 17
<211> 22
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 17
cagctctttt tcaaatctat ac 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
ggctacatac tggagacata gc 22

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19

gctatgtctc cagtatgtag cc 22

<210> 20
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gcagttgcgc ccgtgaacga c 21

<210> 21
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<220>
<223> Description of Artificial Sequence: Primer

<400> 21
gtcgttcacg ggcgcaactg c 21

<210> 22
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<212> DNA
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<223> Description of Artificial Sequence: Primer

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<210> 23
<211> 29
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<220>

<223> Description of Artificial Sequence: Primer

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<210> 24
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 24
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<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gaatctgacg cagagagttc tatgcgc 27

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
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<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
catccccctt gggtgtaatc ag 22

<210> 28
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (15)..(17)
<223> a, g, c or t

<400> 28
cccttccgca tagannngcc tgcgtcagt 29

<210> 29
<211> 29
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (13)..(15)
<223> a, g, c or t

<400> 29
actgacgcag gcnnntctat gcggaaggg 29

<210> 30
<211> 25
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
gcaatcaaat cgctccggat actgc 25

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
gcagtatccg gagcgatttg attgc 25

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ccattccatc aaggttttgg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
ccaaaacctt gatggaatgg 20

<210> 34
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
aaacagggac ccatatggaa gacgc 25

<210> 35
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
aattaactcg aggaatttcg tcatcgctga atacag 36

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
ccctattttc attcctggcc aaaagcactg 30

<210> 37
<211> 550
<212> PRT
<213> Photinus pyralis

<400> 37
Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

```
Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
145                 150                 155                 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
                165                 170                 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
            180                 185                 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
        195                 200                 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
    210                 215                 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
225                 230                 235                 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
                245                 250                 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
            260                 265                 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
        275                 280                 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
    290                 295                 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
305                 310                 315                 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
                325                 330                 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
            340                 345                 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
        355                 360                 365


Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
    370                 375                 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
385                 390                 395                 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
                405                 410                 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
            420                 425                 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
        435                 440                 445
```

```
Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
    450                 455                 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
465                 470                 475                 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
                485                 490                 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
            500                 505                 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
        515                 520                 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
    530                 535                 540

Gly Gly Lys Ser Lys Leu
545                 550
```

<210> 38
<211> 550
<212> PRT
<213> Photinus pyralis

<220>
<221> VARIANT
<222> (214)
<223> xaa=an amino acid other than Thr

<400> 38

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Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
  1               5                  10                  15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
             20                  25                  30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
         35                  40                  45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
     50                  55                  60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 65                  70                  75                  80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
                 85                  90                  95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
            100                 105                 110

Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val
        115                 120                 125
```

```
Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
    130                 135                 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
145                 150                 155                 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
                165                 170                 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
            180                 185                 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
        195                 200                 205

Ala Leu Pro His Arg Xaa Ala Cys Val Arg Phe Ser His Ala Arg Asp
    210                 215                 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
225                 230                 235                 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
                245                 250                 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
            260                 265                 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
        275                 280                 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
    290                 295                 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
305                 310                 315                 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
                325                 330                 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
            340                 345                 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
        355                 360                 365


Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
    370                 375                 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
385                 390                 395                 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
                405                 410                 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
```

```
            420                 425                 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
        435                 440                 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
    450                 455                 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
465                 470                 475                 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
                485                 490                 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
            500                 505                 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
        515                 520                 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
    530                 535                 540

Gly Gly Lys Ser Lys Leu
545                 550


<210> 39
<211> 550
<212> PRT
<213> Photinus pyralis

<220>
<221> VARIANT
<222> (214)
<223> Xaa=Cys, Ala or Asp

<400> 39
Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
  1               5                  10
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